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RAW SEQUENCE LISTING

DATE: 09/26/2001

PATENT APPLICATION: US/09/934,465

TIME: 12:19:50

Input Set : N:\Crf3\RULE60\09934465.txt

Output Set: N:\CRF3\09262001\I934465.raw

5 <110> APPLICANT: Ashkenazi, Avi J.
 9 <120> TITLE OF INVENTION: APO-2 LIGAND
 13 <130> FILE REFERENCE: 11669.22US03
 17 <140> CURRENT APPLICATION NUMBER: 09/934,465
 18 <141> CURRENT FILING DATE: 2001-08-21
 20 <150> PRIOR APPLICATION NUMBER: 08/584,031
 21 <151> PRIOR FILING DATE: 1996-01-09
 23 <160> NUMBER OF SEQ ID NOS: 17
 27 <170> SOFTWARE: PatentIn Ver. 2.0
 31 <210> SEQ ID NO: 1
 33 <211> LENGTH: 281
 35 <212> TYPE: PRT
 37 <213> ORGANISM: Homo sapiens
 41 <400> SEQUENCE: 1

43	Met	Ala	Met	Met	Glu	Val	Gln	Gly	Gly	Pro	Ser	Leu	Gly	Gln	Thr	Cys
45	1				5					10					15	
49	Val	Leu	Ile	Val	Ile	Phe	Thr	Val	Leu	Gln	Ser	Leu	Cys	Val	Ala	
51				20					25					30		
55	Val	Thr	Tyr	Val	Tyr	Phe	Thr	Asn	Glu	Leu	Lys	Gln	Met	Gln	Asp	Lys
57			35					40					45			
61	Tyr	Ser	Lys	Ser	Gly	Ile	Ala	Cys	Phe	Leu	Lys	Glu	Asp	Asp	Ser	Tyr
63			50				55					60				
67	Trp	Asp	Pro	Asn	Asp	Glu	Glu	Ser	Met	Asn	Ser	Pro	Cys	Trp	Gln	Val
69	65				70				75						80	
73	Lys	Trp	Gln	Leu	Arg	Gln	Leu	Val	Arg	Lys	Met	Ile	Leu	Arg	Thr	Ser
75				85					90					95		
79	Glu	Glu	Thr	Ile	Ser	Thr	Val	Gln	Glu	Lys	Gln	Gln	Asn	Ile	Ser	Pro
81				100					105					110		
85	Leu	Val	Arg	Glu	Arg	Gly	Pro	Gln	Arg	Val	Ala	Ala	His	Ile	Thr	Gly
87			115					120					125			
91	Thr	Arg	Gly	Arg	Ser	Asn	Thr	Leu	Ser	Ser	Pro	Asn	Ser	Lys	Asn	Glu
93			130				135					140				
97	Lys	Ala	Leu	Gly	Arg	Lys	Ile	Asn	Ser	Trp	Glu	Ser	Ser	Arg	Ser	Gly
99	145				150					155				160		
103	His	Ser	Phe	Leu	Ser	Asn	Leu	His	Leu	Arg	Asn	Gly	Glu	Leu	Val	Ile
105				165					170					175		
109	His	Glu	Lys	Gly	Phe	Tyr	Tyr	Ile	Tyr	Ser	Gln	Thr	Tyr	Phe	Arg	Phe
111				180					185					190		
115	Gln	Glu	Glu	Ile	Lys	Glu	Asn	Thr	Lys	Asn	Asp	Lys	Gln	Met	Val	Gln
117			195					200					205			
121	Tyr	Ile	Tyr	Lys	Tyr	Thr	Ser	Tyr	Pro	Asp	Pro	Ile	Leu	Leu	Met	Lys
123			210				215					220				
127	Ser	Ala	Arg	Asn	Ser	Cys	Trp	Ser	Lys	Asp	Ala	Glu	Tyr	Gly	Leu	Tyr
129	225				230					235					240	
133	Ser	Ile	Tyr	Gln	Gly	Gly	Ile	Phe	Glu	Leu	Lys	Glu	Asn	Asp	Arg	Ile
135				245					250					255		
139	Phe	Val	Ser	Val	Thr	Asn	Glu	His	Leu	Ile	Asp	Met	Asp	His	Glu	Ala

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141          260          265          270
145 Ser Phe Phe Gly Ala Phe Leu Val Gly
147          275          280
153 <210> SEQ ID NO: 2
155 <211> LENGTH: 1042
157 <212> TYPE: DNA
159 <213> ORGANISM: Homo sapiens
163 <400> SEQUENCE: 2
165 tttcctcact gactataaaa gaatagagaa ggaagggcct cagtgaccgg ctgcctggct 60
167 gacttacagc agtcagactc tgacaggatc atggctatga tggagggtcca ggggggaccc 120
169 agcctgggac agacctgcgt gctgatcgtg atcttcacag tgctcctgca gtctctctgt 180
171 gtggctgtaa cttacgtgta ctttaccaac gagctgaagc agatgcagga caagtactcc 240
173 aaaagtggca ttgcttgttt cttaaaagaa gatgacagtt attgggaccc caatgacgaa 300
175 gagagtatga acagcccctg ctggcaagtc aagtggcaac tccgtcagct cgttagaaag 360
177 atgattttga gaacctctga ggaaaccatt tctacagttc aagaaaagca acaaaatatt 420
179 tctcccctag tgagagaaaag aggtcctcag agagtagcag ctacacataac tgggaccaga 480
181 ggaagaagca acacattgtc ttctccaaac tccaagaatg aaaaggctct gggccgcaaa 540
183 ataaactcct gggaatcatc aaggagtggg cattcattcc tgagcaactt gcacttgagg 600
185 aatggtgaac tggatcatca tgaaaaaggg ttttactaca tctattccca aacatacttt 660
187 cgatttcagg aggaaataaa agaaaacaca aagaacgaca acaaatggtt ccaatatatt 720
189 tacaataaca caagttatcc tgacctata ttgttgatga aaagtgctag aaatagtgtg 780
191 tgggtctaaag atgcagaata tggactctat tccatctatc aagggggaat atttgagctt 840
193 aaggaaaatg acagaatttt tgtttctgta acaaatgagc acttgataga catggaccat 900
195 gaagccagtt ttttcggggc ctttttagtt ggctaactga cctggaaaga aaaagcaata 960
197 acctcaaagt gactattcag ttttcaggat gatacactat gaagatgttt caaaaaatct 1020
199 gaccaaaaac aacaaacaga aa
203 <210> SEQ ID NO: 3
205 <211> LENGTH: 390
207 <212> TYPE: DNA
209 <213> ORGANISM: Homo sapiens
213 <400> SEQUENCE: 3
215 gggaccccaa tgacgaagag agtatgaaca gcccctgctg gcaagtcaag tggcaactcc 60
217 gtcagctcgt tagaaagatg attttgagaa cctctgagga aaccatttct acagttcaag 120
219 aaaagcaaca aaatatttct cccctagtga gagaaagagg tccctcagaga gtacgagctc 180
221 acataactgg gaccagagga agaagcaaca cattgtcttc tccaaactcc aagaatgaaa 240
223 aggtctctgg cgcgaaaata aactcctggg aatcatcaag gagtgggcat tcattcctga 300
225 gcaacttgca cttgaggaat ggtgaactgg tcatccatga aaaagggttt tactacatct 360
227 attcccaaac atactttcga tttcaggagg
231 <210> SEQ ID NO: 4
233 <211> LENGTH: 60
235 <212> TYPE: DNA
237 <213> ORGANISM: Artificial Sequence
241 <220> FEATURE:
243 <221> NAME/KEY: misc_feature
245 <222> LOCATION: (1)..(60)
247 <223> OTHER INFORMATION: Sequence is synthesized
251 <400> SEQUENCE: 4
253 tgacgaagag agtatgaaca gcccctgctg gcaagtcaag tggcaactcc gtcagctcgt 60
257 <210> SEQ ID NO: 5

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Input Set : N:\Crf3\RULE60\09934465.txt
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259 <211> LENGTH: 60
 261 <212> TYPE: DNA
 263 <213> ORGANISM: Artificial Sequence
 267 <220> FEATURE:
 269 <221> NAME/KEY: misc_feature
 271 <222> LOCATION: (1)..(60)
 273 <223> OTHER INFORMATION: Sequence is synthesized
 277 <400> SEQUENCE: 5
 279 ggtgaactgg tcattcatga aaaagggttt tactacatct attcccaaac atactttoga 60
 283 <210> SEQ ID NO: 6
 285 <211> LENGTH: 13
 287 <212> TYPE: PRT
 289 <213> ORGANISM: Artificial Sequence
 293 <220> FEATURE:
 295 <221> NAME/KEY: UNSURE
 297 <222> LOCATION: (1)..(13)
 299 <223> OTHER INFORMATION: Sequence is synthesized
 303 <400> SEQUENCE: 6
 305 Ser Met Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
 307 1 5 10
 313 <210> SEQ ID NO: 7
 315 <211> LENGTH: 27
 317 <212> TYPE: PRT
 319 <213> ORGANISM: Artificial Sequence
 323 <220> FEATURE:
 325 <221> NAME/KEY: UNSURE
 327 <222> LOCATION: (1)..(27)
 329 <223> OTHER INFORMATION: Sequence is synthesized
 333 <400> SEQUENCE: 7
 335 Lys Tyr Ala Leu Ala Asp Ala Ser Leu Lys Met Ala Asp Pro Asn Arg
 337 1 5 10 15
 341 Phe Arg Gly Lys Asp Leu Pro Val Leu Asp Gln
 343 20 25
 349 <210> SEQ ID NO: 8
 351 <211> LENGTH: 24
 353 <212> TYPE: PRT
 355 <213> ORGANISM: Artificial Sequence
 359 <220> FEATURE:
 361 <221> NAME/KEY: UNSURE
 363 <222> LOCATION: (1)..(24)
 365 <223> OTHER INFORMATION: Sequence is synthesized
 369 <400> SEQUENCE: 8
 371 Met Gly His His His His His His His His Ser Ser Gly His
 373 1 5 10 15
 377 Ile Asp Asp Asp Asp Lys His Met
 379 20
 385 <210> SEQ ID NO: 9
 387 <211> LENGTH: 175
 389 <212> TYPE: PRT

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Input Set : N:\Crf3\RULE60\09934465.txt

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391 <213> ORGANISM: Homo sapiens

395 <400> SEQUENCE: 9

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397 Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu
399   1           5           10           15
403 Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser
405           20           25           30
409 Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys
411           35           40           45
415 Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val
417           50           55           60
421 Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly
423   65           70           75           80
427 Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly
429           85           90           95
433 Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu
435           100          105          110
439 Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser
441           115          120          125
445 Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg
447           130          135          140
451 His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg
453  145          150          155          160
457 Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
459           165          170          175

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465 <210> SEQ ID NO: 10

467 <211> LENGTH: 132

469 <212> TYPE: PRT

471 <213> ORGANISM: Homo sapiens

475 <400> SEQUENCE: 10

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477 Val Ser His Arg Tyr Pro Arg Ile Gln Ser Ile Lys Val Gln Phe Thr
479   1           5           10           15
483 Glu Tyr Lys Lys Glu Lys Gly Phe Ile Leu Thr Ser Gln Lys Glu Asp
485           20           25           30
489 Glu Ile Met Lys Val Gln Asn Asn Ser Val Ile Ile Asn Cys Asp Gly
491           35           40           45
495 Phe Tyr Leu Ile Ser Leu Lys Gly Tyr Phe Ser Gln Glu Val Asn Ile
497           50           55           60
501 Ser Leu His Tyr Gln Lys Asp Glu Glu Pro Leu Phe Gln Leu Lys Lys
503   65           70           75           80
507 Val Arg Ser Val Asn Ser Leu Met Val Ala Ser Leu Thr Tyr Lys Asp
509           85           90           95
513 Lys Val Tyr Leu Asn Val Thr Thr Asp Asn Thr Ser Leu Asp Asp Phe
515           100          105          110
519 His Val Asn Gly Gly Glu Leu Ile Leu Ile His Gln Asn Pro Gly Glu
521           115          120          125
525 Phe Cys Val Leu
527           130
533 <210> SEQ ID NO: 11
535 <211> LENGTH: 151

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537 <212> TYPE: PRT
539 <213> ORGANISM: Homo sapiens
543 <400> SEQUENCE: 11
545 Gln Gln Gln Leu Pro Leu Glu Ser Leu Gly Trp Asp Val Ala Glu Leu
547   1           5           10           15
551 Gln Leu Asn His Thr Gly Pro Gln Gln Asp Pro Arg Leu Tyr Trp Gln
553           20           25           30
557 Gly Gly Pro Ala Leu Gly Arg Ser Phe Leu His Gly Pro Glu Leu Asp
559           35           40           45
563 Lys Gly Gln Leu Arg Ile His Arg Asp Gly Ile Tyr Met Val His Ile
565           50           55           60
569 Gln Val Thr Leu Ala Ile Cys Ser Ser Thr Thr Ala Ser Arg His His
571   65           70           75           80
575 Pro Thr Thr Leu Ala Val Gly Ile Cys Ser Pro Ala Ser Arg Ser Ile
577           85           90           95
581 Ser Leu Leu Arg Leu Ser Phe His Phe His Gln Gly Cys Thr Ile Val
583           100          105          110
587 Ser Gln Arg Leu Thr Pro Leu Ala Arg Gly Asp Thr Leu Cys Thr Asn
589           115          120          125
593 Leu Thr Gly Thr Leu Leu Pro Ser Arg Asn Thr Asp Glu Thr Phe Phe
595           130          135          140
599 Gly Val Gln Trp Val Arg Pro
601 145          150
607 <210> SEQ ID NO: 12
609 <211> LENGTH: 148
611 <212> TYPE: PRT
613 <213> ORGANISM: Homo sapiens
617 <400> SEQUENCE: 12
619 Leu Cys Ile Leu Lys Arg Ala Pro Phe Lys Lys Ser Trp Ala Tyr Leu
621   1           5           10           15
625 Gln Val Ala Lys His Leu Asn Lys Thr Lys Leu Ser Trp Asn Lys Asp
627           20           25           30
631 Gly Ile Leu His Gly Val Arg Tyr Gln Asp Gly Asn Leu Val Ile Gln
633           35           40           45
637 Phe Pro Gly Leu Tyr Phe Ile Ile Cys Gln Leu Gln Phe Leu Val Gln
639           50           55           60
643 Cys Pro Asn Asn Ser Val Asp Leu Lys Leu Glu Leu Leu Ile Asn Lys
645   65           70           75           80
649 His Ile Lys Lys Gln Ala Leu Val Thr Val Cys Glu Ser Gly Met Gln
651           85           90           95
655 Thr Lys His Val Tyr Gln Asn Leu Ser Gln Phe Leu Leu Asp Tyr Leu
657           100          105          110
661 Gln Val Asn Thr Thr Ile Ser Val Asn Val Asp Thr Phe Gln Tyr Ile
663           115          120          125
667 Asp Thr Ser Thr Phe Pro Leu Glu Asn Val Leu Ser Ile Phe Leu Tyr
669           130          135          140
673 Ser Asn Ser Asp
675 145
681 <210> SEQ ID NO: 13

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VERIFICATION SUMMARY

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